

SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> A Novel Ligand For FPRL1 And Its Use

<130> G05-0027

<150> JP 2002-324189

<151> 2002-11-07

<150> JP 2002-367119

<151> 2002-12-18

<150> JP 2003-59073

<151> 2003-03-05

<150> JP 2003-191359

<151> 2003-07-03

<150> PCT/JP03/14138

<151> 2003-11-06

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<213> Porcine

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<213> Human

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Leu Gly Val Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile
35 40 45
Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Thr Thr Ile Cys Tyr
50 55 60
Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe
65 70 75 80
Leu Ile Val Ser Met Ala Met Gly Glu Lys Trp Pro Phe Gly Trp Phe
85 90 95
Leu Cys Lys Leu Ile His Ile Val Val Asp Ile Asn Leu Phe Gly Ser
100 105 110
Val Phe Leu Ile Gly Phe Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
115 120 125
His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Met Lys
130 135 140
Val Ile Val Gly Pro Trp Ile Leu Ala Leu Val Leu Thr Leu Pro Val
145 150 155 160
Phe Leu Phe Leu Thr Thr Val Thr Ile Pro Asn Gly Asp Thr Tyr Cys
165 170 175
Thr Phe Asn Phe Ala Ser Trp Gly Gly Thr Pro Glu Glu Arg Leu Lys
180 185 190
Val Ala Ile Thr Met Leu Thr Ala Arg Gly Ile Ile Arg Phe Val Ile
195 200 205
Gly Phe Ser Leu Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile
210 215 220
Ala Ala Lys Ile His Lys Lys Gly Met Ile Lys Ser Ser Arg Pro Leu
225 230 235 240
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro
245 250 255
Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Leu Lys Glu Met Leu

260	265	270
Phe Tyr Gly Lys Tyr Lys Ile Ile Asp Ile Leu Val Asn Pro Thr Ser		
275	280	285
Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe		
290	295	300
Val Gly Gln Asp Phe Arg Glu Arg Leu Ile His Ser Leu Pro Thr Ser		
305	310	315
Leu Glu Arg Ala Leu Ser Glu Asp Ser Ala Pro Thr Asn Asp Thr Ala		
325	330	335
Ala Asn Ser Ala Ser Pro Pro Ala Glu Thr Glu Leu Gln Ala Met		
340	345	350

<210> 3

<211> 1053

<212> DNA

<213> Human

<400> 3

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gtcctgggca atgggcttgt gatctgggtg gctggattcc ggatgacacg cacagtcacc	180
accatctgtt acctgaacct ggccttggt gacttttctt tcacggccac attaccattc	240
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attcacatcg tggtagacat caacctcttt ggaagtgtct tcttgattgg tticattgca	360
ctggaccgct gcatttgtgt cctgcatcca gtctgggccc agaaccaccg cactgtgagt	420
ctggccatga aggtgatcgt cggaccttgg attcttgctc tagtccttac ctigccagtt	480
ttctctttt tgactacagt aactattcca aatggggaca catactgtac tttcaacttt	540
gcatcctggg gtggcacccc tgaggagagg ctgaaggtgg ccattacat gctgacagcc	600
agagggatta tccggtttgt cattggcttt agcttgccga tgtccattgt tgccatctgc	660
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 Tyr Asp Ser Thr Ile Ser Arg Val Leu Trp Ile Leu Thr Met Val Val
 20 25 30
 Leu Ser Ile Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile
 35 40 45
 Trp Val Ala Gly Phe Arg Met Val His Thr Val Thr Thr Thr Cys Phe
 50 55 60
 Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Val Thr Leu Pro Phe
 65 70 75 80
 Phe Val Ile Ser Ile Ala Met Lys Glu Lys Trp Pro Phe Gly Trp Phe
 85 90 95
 Leu Cys Lys Leu Val His Ile Val Val Asp Ile Asn Leu Phe Gly Ser
 100 105 110
 Val Phe Leu Ile Ala Leu Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
 115 120 125
 His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Arg Lys
 130 135 140
 Val Val Val Gly Pro Trp Ile Leu Ala Leu Ile Leu Thr Leu Pro Ile
 145 150 155 160
 Phe Ile Phe Met Thr Thr Val Arg Ile Pro Gly Gly Asn Val Tyr Cys
 165 170 175
 Thr Phe Asn Phe Ala Ser Trp Gly Asn Thr Ala Glu Glu Leu Leu Asn
 180 185 190
 Ile Ala Asn Thr Phe Val Thr Val Arg Gly Ser Ile Arg Phe Ile Ile
 195 200 205
 Gly Phe Ile Met Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile
 210 215 220
 Ala Val Lys Ile His Arg Arg Ala Leu Val Asn Ser Ser Arg Pro Leu

225	230	235	240
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro			
	245	250	255
Phe Gln Leu Val Ala Leu Leu Gly Thr Ile Trp Phe Lys Glu Ser Leu			
	260	265	270
Phe Ser Gly Arg Tyr Lys Ile Leu Asp Met Trp Val His Pro Thr Ser			
	275	280	285
Ser Leu Ala Tyr Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Ala Phe			
	290	295	300
Met Gly Gln Asp Phe His Glu Arg Leu Ile His Ser Leu Pro Ser Ser			
305	310	315	320
Leu Glu Arg Ala Leu Ser Glu Asp Ser Gly Gln Thr Ser Asp Thr Gly			
	325	330	335
Ile Ser Ser Ala Leu Pro Pro Val Asn Ile Asp Ile Lys Ala Ile			
	340	345	350

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<213> Rat

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gcaccttggg gtaacactgc tgaagaacta ttgaacatag ctaacacttt tgtaacagtt	600
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tatggactca tcgctgtcaa gatccacaga agagcacttg ttaattccag ccgtccatta	720
agagtcccta cagcagttgt ggcttccttc tttatctgtt ggtttccctt tcaactggtg	780
gcccttttag gtacaatctg gtttaaagag tcattgttta gtggtcgtta caaaattctt	840

gacatgtggg ttcacccaac cagctcattg gcctacttca atagttgcct caatccaatg 900
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<210> 6

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<212> PRT

<213> Mouse

<400> 6

Met Glu Ser Asn Tyr Ser Ile His Leu Asn Gly Ser Glu Val Val Val
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 Tyr Asp Ser Thr Ile Ser Arg Val Leu Trp Ile Leu Ser Met Val Val
 20 25 30
 Val Ser Ile Thr Phe Phe Leu Gly Val Leu Gly Asn Gly Leu Val Ile
 35 40 45
 Trp Val Ala Gly Phe Arg Met Pro His Thr Val Thr Thr Ile Trp Tyr
 50 55 60
 Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe
 65 70 75 80
 Leu Leu Val Glu Met Ala Met Lys Glu Lys Trp Pro Phe Gly Trp Phe
 85 90 95
 Leu Cys Lys Leu Val His Ile Val Val Asp Val Asn Leu Phe Gly Ser
 100 105 110
 Val Phe Leu Ile Ala Leu Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
 115 120 125
 His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Arg Lys
 130 135 140
 Val Val Val Gly Pro Trp Ile Phe Ala Leu Ile Leu Thr Leu Pro Ile
 145 150 155 160
 Phe Ile Phe Leu Thr Thr Val Arg Ile Pro Gly Gly Asp Val Tyr Cys
 165 170 175
 Thr Phe Asn Phe Gly Ser Trp Ala Gln Thr Asp Glu Glu Lys Leu Asn
 180 185 190
 Thr Ala Ile Thr Phe Val Thr Thr Arg Gly Ile Ile Arg Phe Leu Ile

195	200	205
Gly Phe Ser Met Pro Met Ser Ile Val Ala Val Cys Tyr Gly Leu Ile		
210	215	220
Ala Val Lys Ile Asn Arg Arg Asn Leu Val Asn Ser Ser Arg Pro Leu		
225	230	235
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro		
245	250	255
Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Phe Lys Glu Thr Leu		
260	265	270
Leu Ser Gly Ser Tyr Lys Ile Leu Asp Met Phe Val Asn Pro Thr Ser		
275	280	285
Ser Leu Ala Tyr Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe		
290	295	300
Met Gly Gln Asp Phe Arg Glu Arg Phe Ile His Ser Leu Pro Tyr Ser		
305	310	315
Leu Glu Arg Ala Leu Ser Glu Asp Ser Gly Gln Thr Ser Asp Ser Ser		
325	330	335
Thr Ser Ser Thr Ser Pro Pro Ala Asp Ile Glu Leu Lys Ala Pro		
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<400> 7

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actatctggg atctgaatct agcattggct gacttttctt tcacagcaac tctaccattc	240
cttcttggtg aaatggctat gaaagaaaaa tggccttttg gctggttcct gtgtaaatta	300
gttcacattg tggtagatgt aaacctgttt ggaagtgtct tcttgattgc tctcattgcc	360
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ctggctagga aggtggttgt tgggccctgg atttttgctc tgattctcac ttgcccatt	480
tttatcttct tgactactgt tagaattcct ggaggagatg tgtattgtac attcaacttt	540
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<213> Artificial Sequence

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<223> Primer

<400> 8

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ctttctagat catggggcct ttaactcaat gtc 33

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<210> 11

<211> 27

<212> DNA

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<400> 11

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<210> 12

<211> 24

<212> DNA

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<400> 13

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<210> 14

<211> 43

<212> DNA

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<213> Artificial Sequence

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<210> 16

<211> 13

<212> PRT

<213> Human

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<210> 17

<211> 15

<212> PRT

<213> Porcine

<400> 17

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<211> 16

<212> PRT

<213> Porcine

<400> 18

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<210> 19

<211> 15

<212> PRT

<213> Human

<400> 19

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<210> 20

<211> 16

<212> PRT

<213> Human

<400> 20

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<210> 21

<211> 15

<212> PRT

<213> Porcine

<400> 21

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<210> 22

<211> 15

<212> PRT

<213> Human

<400> 22

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1 5 10 15

<210> 23

<211> 18

<212> PRT

<213> Porcine

<400> 23

Met Thr Asn Ile Arg Lys Ser His Pro Leu Met Lys Ile Ile Asn Asn Ala Phe
1 5 10 15

<210> 24

<211> 18

<212> PRT

<213> Human

<400> 24

Met Thr Pro Met Arg Lys Ile Asn Pro Leu Met Lys Leu Ile Asn His Ser Phe
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